Amendments to the Claims

1. – 29. (Canceled)

30. (Currently Amended) A method of determining the quinolone resistance of an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli, Citrobacter freundii, Enterobacter aerogenes, Enterobacter cloacae, Klebsiella oxytoca, Klebsiella Pneumoniae, Providencia stuartii* and *Serratia marcescens* in a sample, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NOS:9-16, or a complementary sequence thereof, respectively, the presence of hybridization with a nucleic acid indicating the quinolone ~~resistance~~ susceptibility of the respective species.

31. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:9, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Escherichia coli* in the sample.

32. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:10, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Citrobacter freundii* in the sample.

33. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:11, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Enterobacter aerogenes* in the sample.

34. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:12, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Enterobacter cloacae* in the sample.

35. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:13, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Klebsiella oxytoca* in the sample.

36. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:14, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Klebsiella pneumoniae* in the sample.

37. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:15, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Providencia stuartii* in the sample.

38. (Currently Amended) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:16, or a complementary sequence thereof, the presence of hybridization indicating quinolone ~~resistance~~ susceptibility of the *Serratia marcescens* in the sample.